AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings of claims in the application:

LISTING OF CLAIMS:

1-19. (cancelled)

20. **(currently amended)** A protein crystal ~~comprising~~ consisting of: ~~the processivity clamp factor of DNA polymerase,~~ ~~and a peptide of about 3 to about 30 amino acids, in particular~~ ~~of about 16 amino acids, said peptide comprising all or part of~~ ~~the processivity clamp factor binding sequence of a processivity~~ ~~clamp factor interacting protein, such as prokaryotic Pol I, Pol~~ ~~II, Pol III, Pol IV, Pol V, MutS, ligase I, α subunit of DNA~~ ~~polymerase, UmuD or UmuD', or eukaryotic pol ε, pol δ, pol η, pol~~ ~~ι, pol κ,~~

a processivity clamp factor of DNA polymerase that is the β subunit of DNA polymerase polymerase III of *Escherichia coli* and has the amino acid sequence of SEQ ID NO 5; and

a peptide of 16 amino acids having the amino acid sequence of VTLLDPQMERQLVLGL (SEQ ID NO: 1),

wherein said protein crystal is triclinic and has cell dimensions of: a = 41.23 Å, b = 65.22 Å, c = 73.38 Å, α = 73.11°, β = 85.58°, and γ = 85.80°.

21-22. (cancelled)

23. (currently amended) A The protein crystal according to claim 2220, characterized the bysaid protein crystal having atomic coordinates such as obtained by the X-ray diffraction of said protein crystal, said atomic coordinates being represented in Figure 1.

24. (currently amended) A The protein crystal according to claim 2220 or 23, characterized the by thesaid protein crystal having atomic coordinates representing the peptide and the peptide binding site of the β subunit of DNA polymerase III of Escherichia coli, and wherein said atomic coordinates are being as follows:

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ATOM   4045  N   LEU B 155      5.874  17.816  22.109  1.00  1.00      B
ATOM   4046  CA  LEU B 155      6.029  16.359  22.087  1.00  1.00      B
ATOM   4047  CB  LEU B 155      5.055  15.686  23.064  1.00  1.00      B
ATOM   4048  CG  LEU B 155      5.260  16.046  24.536  1.00  1.00      B
ATOM   4049  CD1 LEU B 155      4.256  15.237  25.360  1.00  1.00      B
ATOM   4050  CD2 LEU B 155      6.686  15.757  24.980  1.00  1.00      B
ATOM   4051  C   LEU B 155      5.808  15.776  20.682  1.00  1.00      B
ATOM   4052  O   LEU B 155      6.177  14.521  20.431  1.00  1.00      B
ATOM   4177  N   THR B 172      9.112  11.246  22.902  1.00  1.00      B
ATOM   4178  CA  THR B 172      8.212  10.730  23.917  1.00  1.00      B
ATOM   4179  CB  THR B 172      8.776  11.014  25.344  1.00  1.00      B
ATOM   4180  OG1 THR B 172      7.931  10.400  26.328  1.00  1.00      B
ATOM   4181  CG2 THR B 172      8.870  12.532  25.619  1.00  1.00      B
ATOM   4182  C   THR B 172      6.805  11.269  23.709  1.00  1.00      B
ATOM   4183  O   THR B 172      6.588  12.352  23.145  1.00  1.00      B
ATOM   4192  N   GLY B 174      4.562  10.770  26.397  1.00  1.00      B
ATOM   4193  CA  GLY B 174      3.992  10.745  27.737  1.00  1.00      B
ATOM   4194  C   GLY B 174      3.762   9.337  28.266  1.00  1.00      B
ATOM   4195  O   GLY B 174      3.667   9.141  29.489  1.00  1.00      B
ATOM   4196  N   HIS B 175      3.650   8.349  27.375  1.00  1.00      B
ATOM   4197  CA  HIS B 175      3.440   6.953  27.796  1.00  1.00      B
ATOM   4198  CB  HIS B 175      2.313   6.309  26.977  1.00  1.00      B
ATOM   4199  CG  HIS B 175      0.992   6.997  27.119  1.00  1.00      B
ATOM   4200  CD2 HIS B 175      0.106   7.435  26.193  1.00  1.00      B
ATOM   4201  ND1 HIS B 175      0.420   7.255  28.345  1.00  1.00      B
ATOM   4202  CE1 HIS B 175     -0.763   7.817  28.170  1.00  1.00      B
ATOM   4203  NE2 HIS B 175     -0.977   7.938  26.875  1.00  1.00      B
ATOM   4204  C   HIS B 175      4.706   6.135  27.641  1.00  1.00      B
ATOM   4205  O   HIS B 175      4.990   5.212  28.403  1.00  1.00      B
ATOM   4206  N   ARG B 176      5.481   6.461  26.617  1.00 18.76      B
ATOM   4207  CA  ARG B 176      6.711   5.768  26.422  1.00 18.30      B
ATOM   4208  CB  ARG B 176      6.575   4.633  25.398  1.00 19.53      B
ATOM   4209  CG  ARG B 176      6.329   5.094  23.954  1.00 22.88      B
ATOM   4210  CD  ARG B 176      4.876   4.888  23.657  1.00 22.11      B
ATOM   4211  NE  ARG B 176      4.435   5.312  22.314  1.00 22.09      B
ATOM   4212  CZ  ARG B 176      4.555   4.591  21.202  1.00 20.17      B
ATOM   4213  NH1 ARG B 176      5.159   3.403  21.213  1.00 17.04      B
ATOM   4214  NH2 ARG B 176      3.914   4.977  20.120  1.00 20.02      B
ATOM   4215  C   ARG B 176      7.684   6.807  25.902  1.00 17.30      B
ATOM   4216  O   ARG B 176      7.255   7.860  25.374  1.00 18.10      B
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ATOM	4217	N	LEU	B	177	8.957	6.504	26.080	1.00	17.97	B
ATOM	4218	CA	LEU	B	177	10.049	7.360	25.633	1.00	17.85	B
ATOM	4219	CB	LEU	B	177	10.664	8.095	26.827	1.00	18.29	B
ATOM	4220	CG	LEU	B	177	11.921	8.955	26.611	1.00	16.28	B
ATOM	4221	CD1	LEU	B	177	11.819	10.163	27.559	1.00	19.52	B
ATOM	4222	CD2	LEU	B	177	13.191	8.172	26.839	1.00	19.12	B
ATOM	4223	C	LEU	B	177	11.110	6.517	24.964	1.00	18.45	B
ATOM	4224	O	LEU	B	177	11.291	5.329	25.281	1.00	18.33	B
ATOM	4710	N	PRO	B	242	11.254	17.279	27.890	1.00	1.00	B
ATOM	4711	CD	PRO	B	242	9.987	16.826	27.286	1.00	1.00	B
ATOM	4712	CA	PRO	B	242	11.660	16.404	28.997	1.00	1.00	B
ATOM	4713	CB	PRO	B	242	10.688	15.230	28.874	1.00	1.00	B
ATOM	4714	CG	PRO	B	242	9.448	15.869	28.336	1.00	1.00	B
ATOM	4715	C	PRO	B	242	13.124	15.947	28.987	1.00	1.00	B
ATOM	4716	O	PRO	B	242	13.728	15.748	27.925	1.00	1.00	B
ATOM	4748	N	ARG	B	246	16.133	11.840	33.560	1.00	1.00	B
ATOM	4749	CA	ARG	B	246	15.239	11.808	34.707	1.00	1.00	B
ATOM	4750	CB	ARG	B	246	14.755	13.227	34.984	1.00	1.00	B
ATOM	4751	CG	ARG	B	246	15.880	14.252	35.113	1.00	1.00	B
ATOM	4752	CD	ARG	B	246	16.443	14.295	36.529	1.00	1.00	B
ATOM	4753	NE	ARG	B	246	15.374	14.318	37.524	1.00	1.00	B
ATOM	4754	CZ	ARG	B	246	14.316	15.126	37.477	1.00	1.00	B
ATOM	4755	NH1	ARG	B	246	14.169	15.992	36.481	1.00	1.00	B
ATOM	4756	NH2	ARG	B	246	13.396	15.067	38.430	1.00	1.00	B
ATOM	4757	C	ARG	B	246	14.022	10.889	34.566	1.00	1.00	B
ATOM	4758	O	ARG	B	246	13.384	10.536	35.560	1.00	1.00	B
ATOM	4759	N	VAL	B	247	13.695	10.532	33.327	1.00	1.00	B
ATOM	4760	CA	VAL	B	247	12.553	9.675	33.018	1.00	1.00	B
ATOM	4761	CB	VAL	B	247	12.061	9.942	31.585	1.00	1.00	B
ATOM	4762	CG1	VAL	B	247	10.930	8.991	31.216	1.00	1.00	B
ATOM	4763	CG2	VAL	B	247	11.624	11.391	31.462	1.00	1.00	B
ATOM	4764	C	VAL	B	247	12.962	8.218	33.133	1.00	1.00	B
ATOM	4765	O	VAL	B	247	12.125	7.334	33.308	1.00	1.00	B
ATOM	4996	N	PHE	B	278	-7.702	-1.352	24.244	1.00	1.00	B
ATOM	4997	CA	PHE	B	278	-6.698	-1.155	25.300	1.00	1.00	B
ATOM	4998	CB	PHE	B	278	-7.318	-1.432	26.663	1.00	1.00	B
ATOM	4999	CG	PHE	B	278	-8.431	-0.459	27.021	1.00	1.00	B
ATOM	5000	CD1	PHE	B	278	-8.142	0.882	27.268	1.00	1.00	B
ATOM	5001	CD2	PHE	B	278	-9.760	-0.869	27.021	1.00	1.00	B
ATOM	5002	CE1	PHE	B	278	-9.177	1.816	27.508	1.00	1.00	B
ATOM	5003	CE2	PHE	B	278	-10.795	0.052	27.258	1.00	1.00	B
ATOM	5004	CZ	PHE	B	278	-10.496	1.391	27.500	1.00	1.00	B
ATOM	5005	C	PHE	B	278	-5.403	-1.957	25.131	1.00	1.00	B
ATOM	5006	O	PHE	B	278	-4.356	-1.582	25.677	1.00	1.00	B
ATOM	5332	N	ASN	B	320	0.635	-2.143	27.431	1.00	1.00	B
ATOM	5333	CA	ASN	B	320	-0.051	-1.983	26.158	1.00	1.00	B
ATOM	5334	CB	ASN	B	320	-0.055	-0.504	25.796	1.00	1.00	B
ATOM	5335	CG	ASN	B	320	-0.561	-0.259	24.407	1.00	1.00	B
ATOM	5336	OD1	ASN	B	320	-0.226	-0.997	23.481	1.00	1.00	B
ATOM	5337	ND2	ASN	B	320	-1.362	0.791	24.242	1.00	1.00	B
ATOM	5338	C	ASN	B	320	0.927	-2.745	25.249	1.00	1.00	B
ATOM	5339	O	ASN	B	320	2.093	-2.350	25.102	1.00	1.00	B
ATOM	5353	N	TYR	B	323	2.932	-0.853	22.482	1.00	1.00	B
ATOM	5354	CA	TYR	B	323	4.110	-0.088	22.908	1.00	1.00	B
ATOM	5355	CB	TYR	B	323	3.878	0.590	24.259	1.00	1.00	B
ATOM	5356	CG	TYR	B	323	2.813	1.668	24.294	1.00	1.00	B
ATOM	5357	CD1	TYR	B	323	2.397	2.314	23.127	1.00	1.00	B
ATOM	5358	CE1	TYR	B	323	1.458	3.374	23.170	1.00	1.00	B
ATOM	5359	CD2	TYR	B	323	2.284	2.093	25.509	1.00	1.00	B
ATOM	5360	CE2	TYR	B	323	1.354	3.166	25.567	1.00	1.00	B
ATOM	5361	CZ	TYR	B	323	0.957	3.790	24.399	1.00	1.00	B
ATOM	5362	OH	TYR	B	323	0.112	4.886	24.453	1.00	1.00	B
ATOM	5363	C	TYR	B	323	5.327	-1.018	23.041	1.00	1.00	B
ATOM	5364	O	TYR	B	323	6.468	-0.646	22.726	1.00	1.00	B
ATOM	5519	N	VAL	B	344	3.837	-1.100	39.291	1.00	1.00	B
ATOM	5520	CA	VAL	B	344	3.324	0.227	39.030	1.00	1.00	B
ATOM	5521	CB	VAL	B	344	2.676	0.818	40.318	1.00	1.00	B
ATOM	5522	CG1	VAL	B	344	1.474	-0.026	40.725	1.00	1.00	B
ATOM	5523	CG2	VAL	B	344	3.687	0.847	41.456	1.00	1.00	B
ATOM	5524	C	VAL	B	344	4.405	1.163	38.512	1.00	1.00	B
ATOM	5525	O	VAL	B	344	4.199	2.365	38.405	1.00	1.00	B
ATOM	5532	N	SER	B	346	7.618	2.153	35.615	1.00	21.53	B
ATOM	5533	CA	SER	B	346	8.060	2.002	34.239	1.00	21.50	B
ATOM	5534	CB	SER	B	346	8.655	3.320	33.722	1.00	21.47	B

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ATOM	5535	OG	SER	B	346	9.793	3.703	34.474	1.00	26.08	B
ATOM	5536	C	SER	B	346	9.107	0.914	34.106	1.00	20.70	B
ATOM	5537	O	SER	B	346	9.755	0.521	35.078	1.00	21.55	B
ATOM	5632	N	VAL	B	360	11.730	3.546	27.545	1.00	1.00	B
ATOM	5633	CA	VAL	B	360	11.023	3.501	28.812	1.00	1.00	B
ATOM	5634	CB	VAL	B	360	11.276	4.794	29.641	1.00	1.00	B
ATOM	5635	CG1	VAL	B	360	10.448	4.742	30.934	1.00	1.00	B
ATOM	5636	CG2	VAL	B	360	12.753	4.923	29.937	1.00	1.00	B
ATOM	5637	C	VAL	B	360	9.562	3.381	28.501	1.00	1.00	B
ATOM	5638	O	VAL	B	360	9.008	4.188	27.753	1.00	1.00	B
ATOM	5639	N	VAL	B	361	8.905	2.372	29.069	1.00	19.72	B
ATOM	5640	CA	VAL	B	361	7.488	2.188	28.831	1.00	18.92	B
ATOM	5641	CB	VAL	B	361	7.216	0.872	28.069	1.00	18.99	B
ATOM	5642	CG1	VAL	B	361	5.743	0.769	27.716	1.00	18.31	B
ATOM	5643	CG2	VAL	B	361	8.065	0.839	26.786	1.00	17.76	B
ATOM	5644	C	VAL	B	361	6.793	2.100	30.167	1.00	19.47	B
ATOM	5645	O	VAL	B	361	7.232	1.362	31.038	1.00	16.90	B
ATOM	5646	N	MET	B	362	5.737	2.885	30.318	1.00	1.00	B
ATOM	5647	CA	MET	B	362	4.962	2.882	31.540	1.00	1.00	B
ATOM	5648	CB	MET	B	362	4.226	4.206	31.682	1.00	1.00	B
ATOM	5649	CG	MET	B	362	3.918	4.589	33.122	1.00	1.00	B
ATOM	5650	SD	MET	B	362	5.405	4.806	34.163	1.00	1.00	B
ATOM	5651	CE	MET	B	362	4.575	4.880	35.731	1.00	1.00	B
ATOM	5652	C	MET	B	362	3.949	1.731	31.471	1.00	1.00	B
ATOM	5653	O	MET	B	362	3.385	1.438	30.410	1.00	1.00	B
ATOM	5654	N	PRO	B	363	3.698	1.069	32.599	1.00	1.00	B
ATOM	5655	CD	PRO	B	363	4.521	1.025	33.818	1.00	1.00	B
ATOM	5656	CA	PRO	B	363	2.729	-0.038	32.579	1.00	1.00	B
ATOM	5657	CB	PRO	B	363	3.155	-0.883	33.776	1.00	1.00	B
ATOM	5658	CG	PRO	B	363	3.665	0.160	34.754	1.00	1.00	B
ATOM	5659	C	PRO	B	363	1.272	0.395	32.672	1.00	1.00	B
ATOM	5660	O	PRO	B	363	0.959	1.574	32.811	1.00	1.00	B
ATOM	5661	N	MET	B	364	0.368	-0.568	32.537	1.00	1.00	B
ATOM	5662	CA	MET	B	364	-1.037	-0.272	32.674	1.00	1.00	B
ATOM	5663	CB	MET	B	364	-1.780	-0.391	31.332	1.00	1.00	B
ATOM	5664	CG	MET	B	364	-1.636	-1.670	30.568	1.00	1.00	B
ATOM	5665	SD	MET	B	364	-2.386	-1.510	28.872	1.00	1.00	B
ATOM	5666	CE	MET	B	364	-4.155	-1.253	29.308	1.00	1.00	B
ATOM	5667	C	MET	B	364	-1.602	-1.218	33.725	1.00	1.00	B
ATOM	5668	O	MET	B	364	-0.999	-2.251	34.035	1.00	1.00	B
ATOM	5669	N	ARG	B	365	-2.732	-0.836	34.307	1.00	1.00	B
ATOM	5670	CA	ARG	B	365	-3.383	-1.655	35.324	1.00	1.00	B
ATOM	5671	CB	ARG	B	365	-4.029	-0.756	36.394	1.00	1.00	B
ATOM	5672	CG	ARG	B	365	-4.785	-1.490	37.505	1.00	1.00	B
ATOM	5673	CD	ARG	B	365	-3.859	-2.316	38.398	1.00	1.00	B
ATOM	5674	NE	ARG	B	365	-4.571	-2.956	39.505	1.00	1.00	B
ATOM	5675	CZ	ARG	B	365	-3.984	-3.707	40.434	1.00	1.00	B
ATOM	5676	NH1	ARG	B	365	-2.678	-3.913	40.385	1.00	1.00	B
ATOM	5677	NH2	ARG	B	365	-4.698	-4.247	41.418	1.00	1.00	B
ATOM	5678	C	ARG	B	365	-4.459	-2.492	34.648	1.00	1.00	B
ATOM	5679	O	ARG	B	365	-5.449	-1.961	34.150	1.00	1.00	B
ATOM	5680	N	LEU	B	366	-4.267	-3.801	34.609	1.00	41.59	B
ATOM	5681	CA	LEU	B	366	-5.272	-4.665	33.996	1.00	44.25	B
ATOM	5682	CB	LEU	B	366	-4.615	-5.908	33.366	1.00	45.24	B
ATOM	5683	CG	LEU	B	366	-3.640	-5.701	32.202	1.00	45.46	B
ATOM	5684	CD1	LEU	B	366	-4.331	-5.029	31.031	1.00	47.09	B
ATOM	5685	CD2	LEU	B	366	-2.489	-4.856	32.678	1.00	46.71	B
ATOM	5686	C	LEU	B	366	-6.263	-5.080	35.092	1.00	45.55	B
ATOM	5687	O	LEU	B	366	-6.424	-6.296	35.333	1.00	46.32	B
ATOM	5688	OXT	LEU	B	366	-6.868	-4.169	35.704	1.00	46.33	B
ATOM	5689	CB	ARG	C	10	-5.663	0.205	32.737	0.76	1.00	C
ATOM	5690	CG	ARG	C	10	-7.073	-0.397	32.771	0.76	1.00	C
ATOM	5691	CD	ARG	C	10	-7.748	-0.383	31.408	0.76	1.00	C
ATOM	5692	NE	ARG	C	10	-8.728	-1.462	31.268	0.76	1.00	C
ATOM	5693	CZ	ARG	C	10	-9.992	-1.301	30.875	0.76	1.00	C
ATOM	5694	NH1	ARG	C	10	-10.464	-0.093	30.582	0.76	1.00	C
ATOM	5695	NH2	ARG	C	10	-10.779	-2.365	30.749	0.76	1.00	C
ATOM	5696	C	ARG	C	10	-4.106	2.152	32.497	0.76	1.00	C
ATOM	5697	O	ARG	C	10	-3.278	1.863	33.369	0.76	1.00	C
ATOM	5698	N	ARG	C	10	-6.417	2.186	31.464	0.76	1.00	C
ATOM	5699	CA	ARG	C	10	-5.587	1.727	32.625	0.76	1.00	C
ATOM	5700	N	GLN	C	11	-3.805	2.853	31.408	0.76	1.00	C
ATOM	5701	CA	GLN	C	11	-2.458	3.321	31.094	0.76	1.00	C
ATOM	5702	CB	GLN	C	11	-2.423	3.866	29.662	0.76	1.00	C

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ATOM   5703  CG   GLN C  11    -1.047   4.361  29.231  0.76  1.00      C
ATOM   5704  CD   GLN C  11    -0.039   3.245  29.174  0.76  1.00      C
ATOM   5705  OE1  GLN C  11    -0.263   2.232  28.494  0.76  1.00      C
ATOM   5706  NE2  GLN C  11     1.082   3.415  29.876  0.76  1.00      C
ATOM   5707  C    GLN C  11    -1.895   4.396  32.038  0.76  1.00      C
ATOM   5708  O    GLN C  11    -2.494   5.467  32.217  0.76  1.00      C
ATOM   5709  N    LEU C  12    -0.732   4.111  32.618  0.76  1.00      C
ATOM   5710  CA   LEU C  12    -0.065   5.046  33.519  0.76  1.00      C
ATOM   5711  CB   LEU C  12     0.754   4.277  34.561  0.76  1.00      C
ATOM   5712  CG   LEU C  12    -0.036   3.305  35.450  0.76  1.00      C
ATOM   5713  CD1  LEU C  12     0.907   2.681  36.468  0.76  1.00      C
ATOM   5714  CD2  LEU C  12    -1.184   4.040  36.153  0.76  1.00      C
ATOM   5715  C    LEU C  12     0.845   5.948  32.680  0.76  1.00      C
ATOM   5716  O    LEU C  12     1.111   5.653  31.510  0.76  1.00      C
ATOM   5717  N    VAL C  13     1.317   7.044  33.273  0.76  1.00      C
ATOM   5718  CA   VAL C  13     2.166   7.987  32.543  0.76  1.00      C
ATOM   5719  CB   VAL C  13     1.473   9.371  32.386  0.76  1.00      C
ATOM   5720  CG1  VAL C  13     0.217   9.239  31.523  0.76  1.00      C
ATOM   5721  CG2  VAL C  13     1.113   9.929  33.750  0.76  1.00      C
ATOM   5722  C    VAL C  13     3.542   8.211  33.174  0.76  1.00      C
ATOM   5723  O    VAL C  13     3.740   8.050  34.381  0.76  1.00      C
ATOM   5724  N    LEU C  14     4.498   8.596  32.339  0.76  1.00      C
ATOM   5725  CA   LEU C  14     5.860   8.846  32.803  0.76  1.00      C
ATOM   5726  CB   LEU C  14     6.836   8.819  31.619  0.76  1.00      C
ATOM   5727  CG   LEU C  14     6.972   7.481  30.889  0.76  1.00      C
ATOM   5728  CD1  LEU C  14     7.666   7.705  29.557  0.76  1.00      C
ATOM   5729  CD2  LEU C  14     7.744   6.495  31.769  0.76  1.00      C
ATOM   5730  C    LEU C  14     6.010  10.186  33.517  0.76  1.00      C
ATOM   5731  O    LEU C  14     5.238  11.126  33.284  0.76  1.00      C
ATOM   5732  N    GLY C  15     7.000  10.263  34.396  0.76  1.00      C
ATOM   5733  CA   GLY C  15     7.264  11.510  35.090  0.76  1.00      C
ATOM   5734  C    GLY C  15     8.263  12.275  34.234  0.76  1.00      C
ATOM   5735  O    GLY C  15     9.472  12.210  34.462  0.76  1.00      C
ATOM   5736  N    LEU C  16     7.750  12.995  33.241  0.76  1.00      C
ATOM   5737  CA   LEU C  16     8.576  13.756  32.306  0.76  1.00      C
ATOM   5738  CB   LEU C  16     7.732  14.157  31.094  0.76  1.00      C
ATOM   5739  CG   LEU C  16     7.258  12.955  30.269  0.76  1.00      C
ATOM   5740  CD1  LEU C  16     6.303  13.411  29.171  0.76  1.00      C
ATOM   5741  CD2  LEU C  16     8.467  12.233  29.690  0.76  1.00      C
ATOM   5742  C    LEU C  16     9.263  14.982  32.898  0.76  1.00      C
ATOM   5743  O    LEU C  16    10.182  15.515  32.231  0.76  1.00      C
ATOM   5744  OXT  LEU C  16     8.870  15.398  34.009  0.76  1.00      C
END
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wherein atoms 4045 to 5688 represent the peptide binding site, and atoms 5689 to 5748 represent the peptide of SEQ ID NO 1, said atoms 4045 to 5688 being comprised in the peptide binding site delimited by the amino acids 155 to 364 of the β subunit of DNA polymerase III of *Escherichia coli*, said peptide binding site having the amino acid sequence of SEQ ID NO 7.

25. **(currently amended)** A method to obtain a the protein crystal as defined inof claim 20, said method comprising the following steps:

- mixing a solution of processivity clamp factor of DNA polymerase the β subunit of DNA polymerase polymerase III of

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Escherichia coli having the amino acid sequence of SEQ ID NO 5, with a solution of ~~a~~ the peptide of ~~about 3 to about 30 amino acids, in particular of about~~ 16 amino acids having the amino acid sequence of VTLLDPQMERQLVLGL (SEQ ID NO: 1), ~~said peptide comprising all or part of the processivity clamp factor binding sequence of a processivity clamp factor interacting protein, such as prokaryotic Pol I, Pol II, Pol III, Pol IV, Pol V, MutS, ligase I, α subunit of DNA polymerase, UmuD or UmuD', or eukaryotic pol ε, pol δ, pol η, pol ι, pol κ,~~ and with a solution of ~~MES~~ 2-(N-morpholino)ethane sulfonic acid (MES) at pH 6.0 0.2 M, CaCl₂ 0.2 M, PEG 400 60%, to obtain a crystallisation drop,

— letting the crystallisation drop concentrate against a solution of MES pH 6.0 0.1 M, CaCl₂ 0.1 M, PEG 400 30%, by vapour diffusion, to obtain a protein crystal.

26-37. (cancelled)